

**Amendments to the Claims:**

This listing of claims will replace all prior versions, and listings of claims in the application:

**Listing of Claims:**

- 1-8. (Canceled)
9. (Currently amended) A method for quantification of a target nucleic acid relative to a reference nucleic acid and standardized with a calibrator sample comprising the steps of:
- (a) preparing a common or two separate dilution series of target nucleic acid and reference nucleic acid;
  - (b) amplifying the various dilutions of target nucleic acid and reference nucleic acid under defined reaction conditions, and measuring the amplification of the nucleic acids in real-time;
  - (c) setting defined signal threshold values for the target nucleic acid and reference nucleic acid;
  - (d) determining the cycle numbers  $C_p$  at which the signal threshold values defined for the target nucleic acid and reference nucleic acid are exceeded in each dilution;
  - (e) determining a continuously differentiable function of the  $C_p$  values determined in step d) as a function of the logarithm of the amounts used of target nucleic acid and determining a continuously differentiable function of the  $C_p$  values determined in step d) as a function of the logarithm of the amounts used of reference nucleic acid;
  - (f) determining the  $C_p$  values of the target nucleic acid and reference nucleic acid in a sample to be analysed as well as in a calibrator sample;
  - (g) assigning the  $C_p$  values measured in step f) to particular values of the functions determined in step e);
  - (h) calculating (1) the quotient ~~quotients~~ of the function values from step g) of the target nucleic acid and reference nucleic acid for the sample to be analysed, and (2) the

quotient of the function value from step g) of the target nucleic acid and the reference nucleic acid in as well as for the calibrator sample; and

- (i) determining the ratio of the two quotients from step h) as a measure of the original amount of target nucleic acid contained in the sample to be analysed.

10. (Currently amended) A method for quantification of a target nucleic acid relative to a reference nucleic acid and standardized with a calibrator sample comprising the steps of:

- (a) preparing a common or two separate dilution series of target nucleic acid and reference nucleic acid;
- (b) amplifying the various dilutions of target nucleic acid and reference nucleic acid under defined reaction conditions, and measuring the amplification of the nucleic acids in real-time;
- (c) setting defined signal threshold values for the target nucleic acid and reference nucleic acid;
- (d) determining the cycle numbers  $C_p$  at which the signal threshold values defined for the target nucleic acid and reference nucleic acid are exceeded in each dilution;
- (e) determining a continuously differentiable function of the logarithm of the amounts used of target nucleic acid as a function of the  $C_p$  values determined in step d) and determining a continuously differentiable function of the logarithm of the amounts used of reference nucleic acid as a function of the  $C_p$  values determined in step d);
- (f) determining the  $C_p$  values of the target nucleic acid and reference nucleic acid in a sample to be analysed as well as in a calibrator sample;
- (g) assigning the  $C_p$  values measured in step f) to particular values of the functions determined in step e);
- (h) calculating (1) the quotient ~~quotients~~ of the function values from step g) of the target nucleic acid and reference nucleic acid for the sample to be analysed, and (2) the quotient of the function value from step g) of the target nucleic acid and the reference nucleic acid in as well as for the calibrator sample; and

- (i) determining the ratio of the two quotients from step h) as a measure of the original amount of target nucleic acid contained in the sample to be analysed.
- 11. (Previously presented) The method of claim 10, wherein the continuously differentiable functions from step e) are determined with a polynomial fit.
  - 12. (Previously presented) The method of claim 10, wherein the amplified nucleic acids are detected with at least one fluorescently-labeled hybridization probe.
  - 13. (Previously presented) The method of claim 12, wherein the amplified nucleic acids are detected with FRET hybridization probes, molecular beacons, or TAQMAN<sup>®</sup> probes.
  - 14. (Previously presented) The method of claim 10, wherein the amplified nucleic acids are detected with a DNA-binding dye.